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Additive Main Effects and Multiplicative Interaction (AMMI) Analysis for Yield of Cassava in Nigeria

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Abstract: The problem of genotype-by-environment (G×E) interactions that often complicates the interpretation of multilocal trial analysis making the prediction of genotype performance difficult can be eased with the adoption of the Additive Main Effects and Multiplicative Interaction (AMMI) model analysis. The AMMI model was used in this study to evaluate 20 broad based cassava genotypes established in eight environments in Nigeria in order to; identify stable and adaptable genotypes, determine the magnitude of G×E interaction and identify factors contributing to the G×E interaction pattern. Analysis of variance showed that the effects of environments, genotypes and G×E were highly significant ($p < 0.001$) for storage root yield. AMMI estimates ranked genotypes differently from unadjusted means producing sharper and more stratified rankings. Genotypes 4(2)1425 and 91/02324 was found to be stable and adaptable, 96/0326 was found to be unstable but high yielding, while 96/0590 was highly stable but low yielding. Genotypes 96/0529 and 96/0860 were specifically adapted to Zaria (Northern guinea savanna) and 96/0191 was adapted to Ibadan (forest savanna transition zone). High variation in soil moisture availability was identified as a major causal factor of the interaction observed. Ibadan and Mokwa were relatively stable environments but Mallamadori was highly unstable. Mokwa been highly stable could be considered as a good site for selection broad based improved cassava genotypes.

Key words: Cassava, genotype performance, AMMI, G×E interaction, stability, adaptability

INTRODUCTION

Cassava (*Manihot esculenta* Crantz) is known worldwide as the fourth most important basic food crop after rice, wheat and maize (FAO/FIDA, 2000). It is also a fundamental component in the diet of millions of people and has a wide adaptation to a range of environments (Dixon and Nukenine, 1997). A lot of success has been achieved in the area of breeding cassava to successfully meet the demands of both the farmers and processors (Kawano, 2003). The general breeding scheme for cassava includes evaluating a large number of genotypes at various stages and the testing selected genotypes at several locations. The multi-locational testing however, usually results in genotype-by-environment (G×E) interactions that often complicate the interpretation of results obtained and reduce efficiency in selecting the best genotypes (Annicchiarico and Perenzin, 1994). This interaction is a result of changes in a cultivar's relative performance across environments, due to differential responses of the genotypes to various edaphic, climatic

and biotic factors (Dixon and Nukenine, 1997). The analysis of G×E, therefore, becomes an important tool employed by breeders for evaluating varietal adaptation and also for selecting parents for base populations. The Additive Main Effects and Multiplicative Interaction model (AMMI) was found suitable to handle both the main effects and G×E interactions in multilocal yield trials more effectively and efficiently than other statistical packages (Gauch, 1993).

The AMMI model combines regular analysis of variance for additive effects with principal component analysis (PCA) for multiplicative structure within the interaction. AMMI also provides a visual representation of patterns in the data through a biplot that makes use of the first interaction principal component axis (IPCA1) and the mean yields of both the genotypes and environments (Nachit *et al.*, 1992).

AMMI is, therefore, effective for understanding the G×E interaction, improving the accuracy of yield estimates, increasing the probability of successfully selecting genotypes with the highest yields, imputing

missing data and increasing the flexibility and efficiency of experimental designs (Dixon and Nukenine, 1997). G×E interaction is reportedly large for yield and yield components in cassava to complicate selection (Dixon and Nukenine, 2000). The need therefore to exploit the possibility of identifying genotypes that are less influenced by G×E interaction to help in the selection procedure.

This study therefore make use of the AMMI analysis to determine the pattern of G×E interaction among 20 cassava genotypes evaluated for 2 years in four locations in Nigeria and also to identify genotypes with broad or specific adaptation to the different environments.

MATERIALS AND METHODS

The experiment was conducted in four different agroecological zones in Nigeria for two planting seasons (1999/2000 and 2000/2001). Each agroecology differ for climatic characteristics (Table 1). Genotypes were evaluated in a randomized complete block design with four replicates in a plot size of 40 m² at spacing of 1×1 m. Planting was rainfed and carried out for each location when there was sufficient soil moisture to sustain good plant establishment. Healthy cuttings 25-30 cm long were planted on ridges 30 cm high in a slanting position with two-thirds of the stake length buried in the soil. The fields were maintained free of weeds and neither fertilizer nor herbicides were applied. Storage roots were harvested at 12 months after planting in each agroecology and yield data was based on the two middle rows in each plot.

STATISTICAL ANALYSIS

Analysis of variance (ANOVA) was carried on plot mean basis and pooled over locations and seasons using the Generalized Linear Model (GLM) procedures of the Statistical Analytical System (SAS) version, 2000). The Additive Main effects and Multiplicative Interactions (AMMI) statistical model (MATMODEL 2.0; Gauch, 1993) was used to analyze the yield data. AMMI model produced a biplot that shows both main and interaction effects for both genotypes and environments (Gauch and Zobel, 1996).

The AMMI statistical model equation is:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum \lambda_n y_{gn} \delta_{en} + \rho_{ge} + E_{ger}$$

where:

- Y_{ger} = Yield of genotype g in environment e for replicate r,
- μ = Grand mean,
- α_g = Genotype mean deviations (genotype means minus grand mean),
- β_e = Environment mean deviation,
- n = Number of PCA axes retained in the model,
- λ_n = Singular value for PCA axis n,
- y_{gn} = Genotype eigenvector values for PCA axis n,
- δ_{en} = Environment eigenvector values for PCA axis n,
- ρ_{ge} = Residuals,
- E_{ger} = Error was used.

Table 1: Experimental sites and climatic characteristics

Location	Year		1999/2000		2000/2001	
	Rainfall/month (mm)		Mean temp. (Min) (°C)	Mean temp. (Max) (°C)	Mean temp. (Min) (°C)	Mean temp. (Max) (°C)
Ibadan						
Forest savanna transition	137.33±31.06	108.85±28.83	22.27±0.22	31.53±0.57	21.85±0.30	31.77±0.75
Lat. 7° 26'N						
Long. 3° 54'E						
Mokwa						
Southern guinea savanna	107.38±42.0	97.23±33.85	21.42±0.44	32.38±0.75	21.40±0.45	32.38±0.75
Lat. 9° 29'N						
Long. 5° 04'E						
Zaria						
Northern guinea savanna	79.58±32.91	89.13±30.52	17.09±1.01	31.08±0.71	17.88±1.23	35.62±0.91
Lat. 11° 11'N						
Long. 7° 38'E						
Mallamadori						
Sudan savanna	60.42±24.16	59.96±23.70	19.86±1.21	33.63±1.06	18.31±1.43	36.42±1.85
Lat. 11° 78'N						
Long. 9° 34'E						

Source: Agro climatology unit IITA, Ibadan

RESULTS AND DISCUSSION

There were highly significant ($p < 0.001$) Mean Squares (MS) for storage root yield and root size for all sources of variation (Table 2). Dry matter content and number of roots were not significant for $G \times E$ and for genotype by year. The absence of significant $G \times E$ effects for dry matter has also been reported by Dixon and Nukenine (2000). AMMI analysis in eight environments (Table 3) shows that AMMI analysis partitioned main effects into genotypes, environments and $G \times E$ with all the components showing highly significant effects ($p < 0.001$). The environment had the greatest effect and accounted for 88.9% of the treatment Sum of Squares (SS); genotypes accounted for 2.9% and $G \times E$ interaction had the least effect and accounted for only 8.1% of the treatment SS. The highly significant effects of environment indicate high differential genotypic responses across the different environments. The variation in soil moisture across the different environments was considered as a major underlying causal factor for the $G \times E$ interaction. Environment relative magnitude was much higher than the genotype effect, suggesting that genotype performance is influenced more by environmental factors.

The AMMI biplot provides a visual expression of the relationships between the first interaction principal component axis (IPCA1) and means of genotypes and environments (Fig. 1) with the biplot accounting for up to 95.5% of the treatment sum of squares. The first interaction principal component axis (IPCA1) was highly significant ($p < 0.001$) and explained the interaction pattern better than other interaction axes. The postdictive success for AMMI indicated that the treatment sum of squares was partitioned into two components: 90.1% due to the pattern (genotype main effects and IPCA1) and 9.8% as residual or random variation (noise). The model-validation procedure, therefore, identifies that the 9.8% of the treatment sum of squares allocated to the residual term was not of predictive value. Within environments, AMMI1 frequently ranked genotypes differently from unadjusted means (Table 4). In five out of eight cases, AMMI1 estimation changed the top-yielding entry. Thus, AMMI1 and unadjusted means selected the same winner in three out of eight environments (37.50%), but selected different winners in the remaining five environments (62.50%). With AMMI1 estimates, 91/02324 was ranked first in three environments against four given by the unadjusted means. However, in several but not all cases, this genotype was found among the first three best positions. For example, the unadjusted means ranked it fifth at ENV1 (Ibadan year 1), second in ENV5

Table 2: Mean squares from combined analysis of variance (ANOVA) for storage root yield and other yield components analyzed over 4 locations and 2 years

SV	df	Mean squares			
		No. of roots	Storage root yield (t ha ⁻¹)	Storage root size	Dry matter % (Dm)
Year	1	74.20***	1791.42***	89.57***	487.92***
Loc	3	463.05***	12291.07***	117.35***	4488.32***
Loc*year	3	86.56***	1406.37***	9.04***	225.32***
Rep (Loc*year)	24	5.47***	48.01***	0.80***	55.03***
Clone	19	20.52***	185.30***	2.30***	157.33***
Loc*Clone	57	6.02***	67.18***	1.18***	26.34***
Clone *year	19	2.22ns	26.79***	0.94***	20.27ns
Loc*Clone*year	57	3.11ns	26.14***	0.67***	14.33ns
Error	442	2.79	12.31	0.36	17.11

***Significant level at $p < 0.001$, ns = Not significant

Table 3: AMMI analysis for 20 cassava genotypes grown in 8 environments in Nigeria

Source	df	SS	MS	Probability
Total	638	79216.09	124.16	
TRT	159	61061.89	384.03	0.00***
GEN	19	1766.54	92.97	0.00***
ENV	7	54329.05	7761.29	0.00***
G×E	133	4966.30	37.34	0.00***
IPCA 1	25	2199.44	87.97	0.00***
IPCA 2	23	1123.05	48.82	0.16
IPCA 3	21	473.67	22.55	0.92
Residual	64	1170.13	18.28	0.99
Error	479	18154.19	37.90	

Grand mean 10.823 yield (t ha⁻¹); TRT = Treatment, GEN = Genotype, ENV = Environment; ***Significant at $p < 0.001$

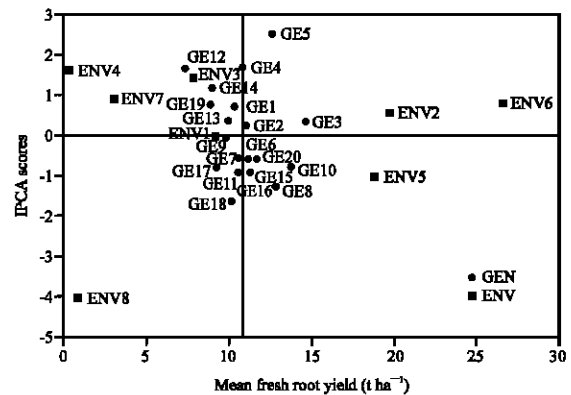


Fig. 1: Biplot of the first AMMI interaction (IPCA) scores (Y-axis) plotted against mean fresh root yield (X-axis) for 20 cassava genotypes in 8 environments in Nigeria;

ENV1 = Ibadan year 1, ENV2 = Mokwa year 1,
 ENV3 = Zaria year 1, ENV4 = Mallamadori year 1;
 ENV5 = Ibadan year 2, ENV6 = Mokwa year 2,
 ENV7 = Zaria year 2, ENV8 = Mallamadori year 2;

Genotypes:
 G1: 30572, G2:4(2)1425, G3:91/02324,
 G4:92/0325, G5:92/0326, G6:95/0166,
 G7:96/0016, G8:96/0037, G9:96/0191,
 G10:96/0249, G11:96/0304, G12:96/0529,
 G13:96/0590, G14:96/0860, G15:96/1039,
 G16:96/1087, G17:96/1439, G18:96/1565,
 G19:96/1632, G20:96/1642

Table 4: Ranking of genotypes following AMMI and unadjusted means for root yield (t ha⁻¹) of 20 genotypes grown in 8 environments

GR	ENV1		ENV2		ENV3		ENV4		ENV5		ENV6		ENV7		ENV8	
	Unadj	AMMI	Unadj	AMMI	Unadj	AMMI	Unadj	AMMI	Unadj	AMMI	Unadj	AMMI	Unadj	AMMI	Unadj	AMMI
1	GE10	GE3	GE3	GE3	GE3	GE5	GE3	GE5	GE8	GE3	GE3	GE5	GE4	GE4	GE8	GE8
2	GE18	GE10	GE13	GE10	GE5	GE3	GE14	GE4	GE3	GE10	GE5	GE3	GE5	GE3	GE10	GE10
3	GE5	GE5	GE10	GE5	GE4	GE4	GE19	GE3	GE7	GE18	GE16	GE16	GE20	GE10	GE18	GE15
4	GE15	GE8	GE5	GE13	GE10	GE10	GE5	GE14	GE20	GE8	GE1	GE1	GE3	GE5	GE15	GE18
5	GE3	GE20	GE9	GE8	GE19	GE2	GE4	GE10	GE5	GE13	GE13	GE11	GE9	GE9	GE11	GE11
6	GE20	GE15	GE2	GE20	GE20	GE14	GE8	GE19	GE16	GE16	GE2	GE13	GE8	GE19	GE6	GE20
7	GE14	GE13	GN8	GE9	GE6	GE8	GE10	GE9	GE10	GE7	GE11	GE2	GE10	GE20	GE16	GE16
8	GE8	GE6	GE17	GE17	GE1	GE20	GE1	GE2	GE18	GE15	GE4	GE10	GE14	GE14	GE20	GE6
9	GE6	GE8	GE7	GE12	GE2	GE1	GE9	GE20	GE11	GE11	GE7	GE7	GE15	GE8	GE3	GE3
10	GE1	GE20	GE12	GE7	GE18	GE19	GE2	GE8	GE13	GE5	GE10	GE18	GE2	GE6	GE17	GE17
11	GE4	GE15	GE6	GE18	GE9	GE6	GE7	GE6	GE15	GE20	GE6	GE8	GE6	GE2	GE9	GE7
12	GE13	GE13	GE15	GE2	GE8	GE9	GE12	GE1	GE1	GE1	GE8	GE4	GE19	GE15	GE7	GE9
13	GE16	GE6	GE20	GE15	GE11	GE15	GE6	GE15	GE6	GE6	GE18	GE6	GE17	GE17	GE2	GE2
14	GE2	GE1	GE1	GE6	GE16	GE7	GE15	GE11	GE12	GE2	GE15	GE15	GE16	GE11	GE19	GE19
15	GE17	GE4	GE18	GE1	GE14	GE11	GE11	GE16	GE17	GE17	GE14	GE12	GE11	GE7	GE1	GE1
16	GE19	GE9	GE4	GE4	GE15	GE13	GE20	GE7	GE12	GE12	GE12	GE20	GE7	GE1	GE13	GE13
17	GE11	GE17	GE14	GE19	GE12	GE16	GE16	GE17	GE9	GE9	GE20	GE14	GE13	GE16	GE14	GE14
18	GE7	GE14	GE11	GE14	GE7	GE12	GE17	GE12	GE19	GE4	GE9	GE19	GE1	GE12	GE4	GE4
19	GE12	GE19	GE16	GE11	GE17	GE17	GE13	GE13	GE4	GE14	GE17	GE17	GE18	GE13	GE5	GE5
20	GE9	GE12	GE19	GE16	GE13	GE18	GE18	GE18	GE14	GE19	GE19	GE9	GE12	GE18	GE12	GE12

Unadjusted mean and AMMI pick the same winner in 3 ENV (37.50%), but they pick different winners in 5 ENV (62.50%). GR = Genotype ranking from top to bottom, Unadj = Unadjusted mean, ENV = Environment

(Ibadan year 2), fourth in ENV7 (Zaria year 2). AMMI ranked it second in ENV3 (Zaria year 1), ENV6 (Mokwa year 2) and ENV7 (Zaria year 2), but third in ENV4 (Mallamadori year 1). However, noise in the unadjusted means elevated some genotypes (such as 96/0037 and 96/0249) to higher positions. Previous research work on yield trials for different crops also showed that AMMI estimates ranked top performing entries differently in more than half of the environments when compared with the unadjusted means in cassava (Dixon and Nukenine, 1997) and maize (Crossa *et al.*, 1990). Therefore, the AMMI estimation for superior genotypes seems more reliable since the discrepancies between AMMI estimates and the unadjusted means were caused by random statistical variation. The AMMI biplot which is a visual expression of the relationships between the first Interaction Principal Component Axis (IPCA) and means of genotypes and environments (Fig. 1) Genotypes or environments located on the same parallel line, relative to the ordinate, have similar yield, while those located on the right side of the midpoint of the axis has higher yields than those on the left hand side. The biplot showed four groupings of genotypes; 96/0529, generally low yielding and unstable; 96/0590 and 96/1632, low yielding and moderately stable; 4(2)1425 and 91/02324, high yielding and stable; 92/0326, high yielding but unstable. Genotypes 30572, 4(2)1425 and 91/02324 were highly stable across environments with 4(2)1425 the most stable and also high yielding; 96/0590, although highly stable, was not very productive in storage root yield. Genotype 92/0326 was highly productive with regard to root yield but highly unstable. Genotypes with IPCA1 scores near zero had little

Table 5: AMMI mean yield and IPCA 1 scores for 20 cassava genotypes grown in 8 environments

Genotypes	ID	AMMI mean yield (t ha ⁻¹)	IPCA 1 Score	
30572	GEN1	10.34	0.67	
4(2)1425	GEN2	11.03	0.20	
91/02324	GEN3	14.61	0.33	
92/0325	GEN4	10.86	1.67	
92/0326	GEN5	12.66	2.47	
95/0166	GEN6	11.17	-0.61	
96/0016	GEN7	10.57	-0.57	
96/0037	GEN8	12.84	-1.29	
96/0191	GEN9	9.90	-0.10	
96/0249	GEN10	13.71	-0.79	
96/0304	GEN11	10.55	-0.95	
96/0529	GEN12	7.37	1.64	
96/0590	GEN13	9.96	0.34	
96/0860	GEN14	8.98	1.14	
96/1039	GEN15	11.28	-0.94	
96/1087	GEN16	10.64	-0.94	
96/1439	GEN17	9.29	-0.76	
96/1565	GEN18	10.17	-1.65	
96/1632	GEN19	8.87	0.75	
96/1642	GEN20	11.68	-0.60	
Environments				
Ibadan	Year 1	ENV1	9.26	-0.06
Mokwa	Year 1	ENV2	19.77	0.52
Zaria	Year 1	ENV3	7.89	1.40
Mallamadori	Year 1	ENV4	0.30	1.57
Ibadan	Year 2	ENV5	18.86	-1.05
Mokwa	Year 2	ENV6	26.67	0.80
Zaria	Year 2	ENV7	3.00	0.86
Mallamadori	Year 2	ENV8	0.81	-4.03

interaction across environments while genotypes with very high IPCA1 values had considerable interactions across environments. Of the 20 genotypes, eight had negligible interactions characterized by low IPCA scores 30572, 4(2)1425, 91/02324, 95/0166, 96/0016, 96/0191, 96/0590 and 96/1642 (Table 5) and are relatively stable

showing broad adaptation across environments. Six genotypes with higher IPCA scores were highly interactive and were unstable across environments; these were 92/0325, 92/0326, 96/0037, 96/0529, 96/0860 and 96/1565. The underlying causes of the interaction observed can therefore be based on both the genetic differences between these genotypes and the different environments (Wallace *et al.*, 1995). Mokwa was more stable than Ibadan and had the best performances for root yield. Both locations were relatively stable environments and highly productive for root yield. Zaria and Mallamadori, both in the drier Northern part of the country, were both characterized with lower root yield that was mainly due to the harsh climatic conditions experienced there. The long growing period and varied agroecological conditions in which cassava is cultivated expose the crop to numerous biotic and abiotic stresses, a combination of which result in devastating effects on the yield. During the dry season, which lasts for more than 6 months in the Sudan savanna, the combined effect of termite attack on the plants coupled with the lack of moisture further aggravates the serious yield losses. Cock (1985) noted that stability in field performance of genotypes is influenced by prevailing biotic and abiotic stresses. Resistance to biotic stresses and tolerance to abiotic factors will ensure a high-level performance. Therefore, identifying genotypes that can tolerate prolonged drought conditions will lead to improved yield, especially in the drought-prone areas of the arid and semi-arid parts of Africa.

In the second season, the performance in storage root yield of genotypes was better than in the first season. Four genotypes (91/02324, 96/0249, 96/0037 and 92/0326) with root yields above 12.0 t ha⁻¹ were categorized as high yielding, ten genotypes with root yields between 12.0 and 10.0 t ha⁻¹ had moderate root yield, four genotypes (96/0529, 96/0860, 96/1439 and 96/1632) with yields of less than 10 (t ha⁻¹) were considered low yielding. Genotypes 96/0529 and 96/0860 were found to be specifically adapted to Zaria; 96/0191 was specifically adapted to Ibadan. Ibadan and Mokwa were favourable environments, but Zaria and Mallamadori were less favourable.

CONCLUSIONS

The AMMI statistical model has been used to diagnose the G×E interaction pattern of fresh storage root yield of cassava. Genotypes 30572, 4(2)1425 and 91/02324 showed broad adaptation. They were hardly affected by the G×E interaction and thus will perform well across a wide range of environments. Mokwa with a relatively stable genotype performance could be regarded as good

selection sites for identifying broad based and adaptable cassava genotypes and for other improvement work on cassava.

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